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RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/741,843

TIME: 15:31:38

Input Set : A:\MS.txt

Output Set: N:\CRF3\10292001\I741843.raw

3 <110> APPLICANT: LEUNG, Shui-on
 4 HANSEN, Hans
 6 <120> TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA

7 AND LEUKEMIA CELLS
 9 <130> FILE REFERENCE: 018733/0996
 11 <140> CURRENT APPLICATION NUMBER: US 09/741,843
 12 <141> CURRENT FILING DATE: 2000-12-22
 14 <150> PRIOR APPLICATION NUMBER: US 09/127,902
 15 <151> PRIOR FILING DATE: 1998-08-03
 17 <150> PRIOR APPLICATION NUMBER: US 08/690,102
 18 <151> PRIOR FILING DATE: 1996-07-06
 20 <150> PRIOR APPLICATION NUMBER: US 08/289,576
 21 <151> PRIOR FILING DATE: 1994-08-12
 23 <160> NUMBER OF SEQ ID NOS: 21
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 339

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 30 <213> ORGANISM: Murinae gen. sp.
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(339)
 35 <223> OTHER INFORMATION:
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39	gac att cag ctg acc cag tct cca tca tct ctg gct gtg tct gca gga	48
40	Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly	
41	1 5 10 15	
43	gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt	96
44	Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
45	20 25 30	
47	gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag	144
48	Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
49	35 40 45	
51	tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc	192
52	Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
53	50 55 60	
55	cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc	240
56	Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
57	65 70 75 80	
59	atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa	288
60	Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln	
61	85 90 95	
63	tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa	336
64	Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
65	100 105 110	
67	cgt	339
68	Arg	

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74 <212> TYPE: PRT
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83 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
84 20 25 30
87 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
88 35 40 45
91 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
92 50 55 60
95 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
96 65 70 75 80
99 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
100 85 90 95
103 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
104 100 105 110
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111 <210> SEQ ID NO: 3
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114 <213> ORGANISM: Murinae gen. sp.
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117 <221> NAME/KEY: CDS
118 <222> LOCATION: (1)..(348)
119 <223> OTHER INFORMATION:
122 <400> SEQUENCE: 3
123 cag gtc cag ctg cag gag tca ggg gct gaa ctg tca aaa cct ggg gcc 48
124 Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
125 1 5 10 15
127 tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
128 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
129 20 25 30
131 tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144
132 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
133 35 40 45
135 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
136 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
137 50 55 60
139 aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240
140 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
141 65 70 75 80
143 atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288
144 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
145 85 90 95
147 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc 336
148 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu

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151 aca gtc tcc tcg
152 Thr Val Ser Ser
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157 <211> LENGTH: 116
158 <212> TYPE: PRT
159 <213> ORGANISM: Murinae gen. sp.
161 <400> SEQUENCE: 4
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164 1          5          10          15
167 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
168          20          25          30
171 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
172          35          40          45
175 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
176          50          55          60
179 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
180 65          70          75          80
183 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
184          85          90          95
187 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
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191 Thr Val Ser Ser
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195 <210> SEQ ID NO: 5
196 <211> LENGTH: 339
197 <212> TYPE: DNA
198 <213> ORGANISM: Homo sapiens
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(339)
203 <223> OTHER INFORMATION:
206 <400> SEQUENCE: 5
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209 1          5          10          15
211 gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt
212 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
213          20          25          30
215 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa
216 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
217          35          40          45
219 gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc
220 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
221          50          55          60
223 cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc
224 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
225 65          70          75          80

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227 atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa      288
228 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
229           85                      90                      95
231 tac ctc tcc tgc tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa      336
232 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
233           100                      105                      110
235 cgt      339
236 Arg
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 113
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
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247 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
248 1           5                      10                      15
251 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
252           20                      25                      30
255 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
256           35                      40                      45
259 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
260           50                      55                      60
263 Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
264 65           70                      75                      80
267 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
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271 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
272           100                      105                      110
275 Arg
279 <210> SEQ ID NO: 7
280 <211> LENGTH: 348
281 <212> TYPE: DNA
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
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286 <222> LOCATION: (1)..(348)
287 <223> OTHER INFORMATION:
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292 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
293 1           5                      10                      15
295 tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
296 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
297           20                      25                      30
299 tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att      144
300 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
301           35                      40                      45
303 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc      192
304 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
305           50                      55                      60

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307 aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac      240
308 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
309 65                               70                               75                               80
311 atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt      288
312 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
313                               85                               90                               95
315 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc      336
316 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
317                               100                              105                              110
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320 Thr Val Ser Ser
321      115
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 116
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
329 <400> SEQUENCE: 8
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332 1                               5                               10                               15
335 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
336                               20                               25                               30
339 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
340                               35                               40                               45
343 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
344                               50                               55                               60
347 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
348 65                               70                               75                               80
351 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
352                               85                               90                               95
355 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
356                               100                              105                              110
359 Thr Val Ser Ser
360      115
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364 <211> LENGTH: 116
365 <212> TYPE: PRT
366 <213> ORGANISM: Homo sapiens
368 <400> SEQUENCE: 9
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371 1                               5                               10                               15
374 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
375                               20                               25                               30
378 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
379                               35                               40                               45
382 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
383                               50                               55                               60
386 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
387 65                               70                               75                               80
390 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys

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VERIFICATION SUMMARY

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